

GenCore version 5.1.7
 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: April 3, 2006, 08:26:10 ; Search time 78.5658 Seconds
 (without alignments) 3345.152 Million cell updates/sec

Title: US-10-715-667-21

Perfect score: 3334

Sequence: 1 MNQVTLQWDAVIALYIIPSW.....TYFPQNLIESHNFRISLEK 629

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 100 summaries

Database : Published Applications_NA_Main:*

1: /cgnd_6/prodata/1/pubpaas/US07_PUBCOMB.pep:*

2: /cgnd_6/prodata/1/pubpaas/US08_PUBCOMB.pep:*

3: /cgnd_6/prodata/1/pubpaas/US09_PUBCOMB.pep:*

4: /cgnd_6/prodata/1/pubpaas/US10_PUBCOMB.pep:*

5: /cgnd_6/prodata/1/pubpaas/US10B_PUBCOMB.pep:*

6: /cgnd_6/prodata/1/pubpaas/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	3334	100 0	629	3 US-09-972-718-21
2	3334	100 0	629	4 US-10-105-930-10
3	3334	100 0	629	4 US-10-715-667-21
4	3314	99 4	629	3 US-09-853-10-2
5	3314	99 4	629	5 US-10-797-15-6
6	3314	99 4	629	5 US-10-720-0-2
7	3314	99 4	629	5 US-10-667-219-2
8	3314	99 4	629	5 US-10-667-219-2
9	3312	99 3	629	4 US-10-667-219-2
10	2972	89 1	565	3 US-09-972-708-23
11	2972	89 1	644	4 US-10-715-667-23
12	2278	68 3	644	4 US-09-972-708-2
13	2278	68 3	644	4 US-10-715-667-2
14	2212	66 3	428	4 US-10-105-930-8
15	2195	65 6	428	4 US-10-105-930-6
16	2037	61 1	384	3 US-09-972-708-26
17	2037	61 1	384	4 US-10-247-443-2
18	2037	61 1	384	4 US-10-715-667-26
19	2037	61 1	384	6 US-11-016-16-2
20	1888	56 6	356	3 US-09-972-708-25
21	1888	56 6	356	4 US-10-105-930-4
22	1715	51 4	337	4 US-10-105-930-2
23	1020	30 6	344	3 US-09-972-708-16
24	1020	30 6	344	4 US-10-715-667-16
25	293	8 8	52	4 US-10-105-930-24
26	262	7 9	46	4 US-10-105-930-28
27	232	7 0	951	5 US-09-972-708-9

28	232	7 0	951	3 US-09-935-968-9
29	232	7 0	951	4 US-10-287-035-9
30	232	7 0	951	4 US-10-282-162-9
31	232	7 0	951	6 US-11-134-114-9
32	227	6 8	861	4 US-10-398-666-12
33	224	6 7	861	4 US-10-105-930-27
34	222	6 7	862	3 US-09-853-180-5
35	222	6 7	862	5 US-10-797-157-7
36	222	6 7	862	5 US-10-370-715B-68
37	222	6 7	862	5 US-10-720-0-36-4
38	222	6 7	862	5 US-10-667-289-4
39	222	6 7	862	5 US-10-667-290-4
40	222	6 6	859	3 US-09-313-942-7
41	220	6 6	859	3 US-09-853-180-4
42	220	6 6	859	4 US-10-287-035-7
43	220	6 6	859	4 US-10-287-035-7
44	220	6 6	859	4 US-10-287-035-7
45	215	6 4	918	4 US-09-853-180-4
46	215	6 4	918	3 US-09-313-942-7
47	215	6 4	918	3 US-09-829-72A-9
48	215	6 4	918	4 US-10-177-293-230
49	215	6 4	918	4 US-10-295-0-77-74
50	215	6 4	918	4 US-10-058-270A-32
51	215	6 4	918	4 US-10-715-667-8
52	215	6 4	918	5 US-10-720-0-26-3
53	215	6 4	918	5 US-10-667-289-3
54	215	6 4	918	5 US-11-667-290-3
55	214	6 4	918	6 US-11-067-211-5
56	213	6 4	918	3 US-09-313-942-10
57	213	6 4	918	3 US-09-935-868-10
58	213	6 4	918	4 US-10-287-035-10
59	213	6 4	918	4 US-10-282-162-10
60	213	6 4	918	6 US-11-134-114-10
61	213	6 4	918	5 US-10-850-210-6
62	212	6 4	708	4 US-10-313-135-2
63	210	6 3	1158	3 US-09-935-868-26
64	210	6 3	1158	3 US-09-935-868-26
65	210	6 3	1158	4 US-10-287-035-26
66	210	6 3	1158	4 US-10-282-162-26
67	210	6 3	1158	6 US-11-134-114-26
68	210	6 3	1168	3 US-09-313-942-24
69	210	6 3	1168	3 US-09-935-868-24
70	210	6 3	1168	4 US-10-287-035-24
71	210	6 3	1168	4 US-10-282-162-24
72	210	6 3	1168	4 US-11-134-114-24
73	208	6 2	1168	4 US-10-935-868-426
74	208	6 2	1168	5 US-10-884-443-1
75	208	6 2	1168	5 US-10-311-473-12
76	208	6 2	1168	4 US-10-755-625-5
77	208	6 2	1168	4 US-10-105-930-29
78	196	5 9	1168	3 US-09-864-761-48948
79	194	5 8	1097	3 US-09-972-0-08-6
80	194	5 8	1097	4 US-10-715-667-6
81	194	5 8	1119	4 US-10-276-774-2630
82	192	5 8	1119	4 US-10-932-708-14
83	192	5 8	1119	4 US-10-056-265-2
84	192	5 8	1119	4 US-10-715-667-14
85	191	5 7	649	3 US-09-892-949-46
86	191	5 7	649	4 US-10-351-157-109
87	191	5 7	649	4 US-10-272-531-46
88	191	5 7	649	5 US-10-982-555-46
89	191	5 7	649	5 US-10-982-555-46
90	191	5 7	649	5 US-10-982-555-46
91	191	5 7	649	5 US-10-066-265-17
92	191	5 7	662	4 US-10-351-157-5
93	191	5 7	662	4 US-10-352-531-5
94	191	5 7	662	4 US-10-772-331-54
95	191	5 7	662	4 US-10-715-667-15
96	191	5 7	662	5 US-10-982-555-46
97	191	5 7	732	3 US-09-892-949-2
98	191	5 7	732	4 US-10-351-157-111
99	191	5 7	732	4 US-10-772-531-2
100	191	5 7	732	5 US-10-982-555-2

5	732	4	732	4 US-10-772-531-2
5	732	4	732	5 US-10-982-555-2
5	951	3	951	3 US-09-935-868-9
3	951	4	951	4 US-10-287-035-9
3	951	4	951	4 US-10-282-162-9
3	951	6	951	6 US-11-134-114-9
3	951	6	951	6 US-10-398-666-12
3	951	7	951	7 US-10-105-930-27
3	951	8	951	8 US-09-853-180-5
3	951	9	951	9 US-10-935-868-26
3	951	10	951	10 US-10-287-035-7
3	951	11	951	11 US-10-287-035-7
3	951	12	951	12 US-10-311-473-12
3	951	13	951	13 US-10-755-625-5
3	951	14	951	14 US-10-056-265-2
3	951	15	951	15 US-10-715-667-14
3	951	16	951	16 US-09-892-949-54
3	951	17	951	17 US-10-066-265-17
3	951	18	951	18 US-10-351-157-5
3	951	19	951	19 US-10-352-531-5
3	951	20	951	20 US-10-772-331-54
3	951	21	951	21 US-10-715-667-15
3	951	22	951	22 US-09-892-949-2
3	951	23	951	23 US-09-892-949-2
3	951	24	951	24 US-10-351-157-111
3	951	25	951	25 US-10-772-531-2
3	951	26	951	26 US-10-982-555-46
3	951	27	951	27 US-10-982-555-46
3	951	28	951	28 US-10-982-555-46
3	951	29	951	29 US-10-982-555-46

ALIGNMENTS

RESULT 1
US-09-972-708-21
Sequence 21, Application US/09972708
Publication No. US20030059871A1
GENERAL INFORMATION:
APPLICANT: Immunex Corporation
APPLICANT: Cosman, David J.
APPLICANT: Mosley, Bruce A.
APPLICANT: Bird, Timothy A.
APPLICANT: DuBois, Robert P.
APPLICANT: Wiley, Steven R.
TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPR1 AND HPR2
FILE REFERENCE: 3160-B
CURRENT APPLICATION NUMBER: US/09/972,708
CURRENT FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn version 3.1
SEQ ID NO 21
LENGTH: 629
TYPE: PRT
ORGANISM: Homo sapiens
US-09-972-708-21

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

GenCore version 5.1.7
 Copyright (c) 1993 - 2006 Biocceleration Ltd.

On protein - protein search, using sw model

Run on: April 3, 2006, 08:26:10 ; (without alignments) Search time 44.4665 Seconds

3345.152 Million cell updates/sec

Title: US-10-715-667-25

Perfect score: 1934

Sequence: 1 MNQVTTQMDAVIALYIIFSW. TVASISRGHTLSQIKEGSY 356

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 100 summaries

Database : Published_Applications_AA_Main:*

1: /cgmn2_6/prodata/1/pupaa/US07_PUBCOMB.pep:*

2: /cgmn2_6/prodata/1/pupaa/US08_PUBCOMB.pep:*

3: /cgmn2_6/prodata/1/pupaa/US09_PUBCOMB.pep:*

4: /cgmn2_6/prodata/1/pupaa/US10_PUBCOMB.pep:*

5: /cgmn2_6/prodata/1/pupaa/US11_PUBCOMB.pep:*

6: /cgmn2_6/prodata/1/pupaa/US11_PUBCOMB.pep:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1934	100.0	356	3 US-09-972-708-25
2	1934	100.0	356	4 US-10-715-667-25
3	1888	97.6	428	4 US-10-105-930-8
4	1888	97.6	629	3 US-09-972-708-21
5	1888	97.6	629	4 US-10-105-930-10
6	1888	97.6	629	4 US-10-715-667-21
7	1881	97.3	384	3 US-09-972-708-26
8	1881	97.3	384	4 US-10-247-453-2
9	1881	97.3	384	4 US-10-720-036-26
10	1881	97.3	384	6 US-11-016-16-2
11	1871	96.7	428	4 US-10-105-930-4
12	1871	96.7	629	4 US-10-105-930-6
13	1868	96.6	629	3 US-09-853-180-2
14	1868	96.6	629	5 US-10-797-157-6
15	1868	96.6	629	5 US-10-720-036-2
16	1868	96.6	629	5 US-10-667-289-2
17	1868	96.6	629	5 US-10-667-230-2
18	1732	89.6	565	3 US-09-972-708-23
19	1732	89.6	565	4 US-10-715-667-23
20	1715	88.7	337	4 US-10-105-930-2
21	1477.5	73.3	644	3 US-09-720-036-27
22	1477.5	73.3	644	4 US-10-715-667-27
23	1020.5	52.8	344	3 US-09-972-708-16
24	1020.5	52.8	344	4 US-10-715-667-16
25	293	15.1	52	4 US-10-105-930-24
26	262	13.5	46	4 US-10-105-930-28
27	11.7	4	861	4 US-10-398-666-12

28	224	11.6	39	4 US-10-105-930-27
29	222	11.5	862	3 US-09-853-180-5
30	222	11.5	862	5 US-10-797-157-7
31	222	11.5	862	5 US-10-720-036-4
32	222	11.5	862	5 US-10-667-289-4
33	222	11.5	862	5 US-10-667-230-4
34	222	11.5	862	5 US-10-667-288-7
35	215.5	11.1	859	3 US-09-313-942-7
36	215.5	11.1	859	3 US-09-935-888-9
37	215.5	11.1	859	4 US-10-287-035-9
38	215.5	11.1	859	4 US-10-282-162-10
39	215.5	11.1	859	6 US-11-134-14-9
40	213	11.0	859	6 US-11-134-14-7
41	215.5	11.1	951	3 US-09-935-888-10
42	215.5	11.1	951	4 US-10-287-035-10
43	213	11.0	918	4 US-10-282-162-10
44	215.5	11.1	951	6 US-11-134-14-10
45	213	11.0	918	3 US-09-853-180-4
46	212.5	11.0	918	3 US-09-972-708-8
47	213	11.0	918	3 US-09-829-472-9
48	213	11.0	918	4 US-10-287-035-10
49	213	11.0	918	6 US-11-134-14-10
50	212.5	11.0	918	3 US-09-853-180-4
51	212.5	11.0	918	3 US-09-972-708-8
52	212.5	11.0	918	3 US-09-829-472-9
53	212.5	11.0	918	4 US-10-177-93-230
54	212.5	11.0	918	4 US-10-295-027-74
55	212.5	11.0	918	4 US-10-715-667-8
56	212.5	11.0	918	5 US-10-720-036-3
57	212.5	11.0	918	5 US-10-850-210-6
58	212.5	11.0	918	5 US-10-667-288-3
59	212.5	11.0	918	5 US-10-667-290-3
60	212.5	11.0	918	4 US-10-313-135-2
61	211.5	10.9	918	6 US-11-067-8-51-5
62	211.5	10.9	918	6 US-10-755-889-426
63	208	10.8	329	5 US-10-884-043-1
64	208	10.8	488	4 US-10-079-625-5
65	207.5	10.7	807	4 US-10-311-473-12
66	207.5	10.7	1158	3 US-09-313-942-26
67	207.5	10.7	1158	3 US-09-935-668-26
68	207.5	10.7	1158	3 US-10-282-162-26
69	207.5	10.7	1158	4 US-10-287-162-26
70	207.5	10.7	1158	4 US-11-134-14-26
71	207.5	10.7	1158	6 US-11-134-14-26
72	207.5	10.7	1168	3 US-09-313-942-24
73	207.5	10.7	1168	3 US-09-935-888-24
74	207.5	10.7	1168	4 US-10-287-135-24
75	207.5	10.7	1168	4 US-10-282-162-24
76	207.5	10.7	1168	6 US-11-134-14-24
77	197	10.2	34	4 US-10-105-930-29
78	196	10.1	36	3 US-09-864-761-48948
79	165.6	9.6	837	4 US-10-659-295-35
80	186.5	9.6	837	5 US-10-880-101A-35
81	182	9.4	1097	4 US-09-972-708-6
82	9.4	1097	4 US-10-715-667-6	
83	182	9.4	1119	4 US-10-276-774-2690
84	170	8.8	836	3 US-09-972-708-9
85	170	8.8	836	4 US-10-659-295-34
86	170	8.8	836	4 US-10-715-667-9
87	170	8.8	836	5 US-10-880-101A-34
88	167.5	8.7	603	4 US-10-105-930-27
89	167	8.6	385	3 US-09-880-578-19
90	167	8.6	405	3 US-09-753-684-2
91	167	8.6	405	4 US-10-074-901-2
92	167	8.6	413	3 US-09-037-577-13
93	167	8.6	425	3 US-09-377-657-15
94	167	8.6	425	3 US-09-377-657-15
95	163.5	8.5	303	3 US-09-880-578-21
96	163.5	8.5	303	3 US-09-880-578-21
97	163.5	8.5	389	3 US-09-880-578-27
98	163.5	8.5	389	3 US-09-880-578-29
99	163.5	8.5	422	3 US-09-880-578-29
100	163	8.4	407	4 US-10-247-463-5

Sequence 27, Appli	Sequence 5, Appli
Sequence 7, Appli	Sequence 6, Appli
Sequence 7, Appli	Sequence 7, Appli
Sequence 7, Appli	Sequence 9, Appli
Sequence 7, Appli	Sequence 10, Appli
Sequence 7, Appli	Sequence 10, Appli
Sequence 9, Appli	Sequence 4, Appli
Sequence 9, Appli	Sequence 10, Appli
Sequence 9, Appli	Sequence 10, Appli
Sequence 10, Appli	Sequence 10, Appli
Sequence 10, Appli	Sequence 10, Appli
Sequence 11, Appli	Sequence 11, Appli
Sequence 12, Appli	Sequence 12, Appli
Sequence 12, Appli	Sequence 12, Appli
Sequence 13, Appli	Sequence 13, Appli
Sequence 14, Appli	Sequence 14, Appli
Sequence 15, Appli	Sequence 15, Appli
Sequence 16, Appli	Sequence 16, Appli
Sequence 17, Appli	Sequence 17, Appli
Sequence 18, Appli	Sequence 18, Appli
Sequence 19, Appli	Sequence 19, Appli
Sequence 20, Appli	Sequence 20, Appli
Sequence 21, Appli	Sequence 21, Appli
Sequence 22, Appli	Sequence 22, Appli
Sequence 23, Appli	Sequence 23, Appli
Sequence 24, Appli	Sequence 24, Appli
Sequence 25, Appli	Sequence 25, Appli
Sequence 26, Appli	Sequence 26, Appli
Sequence 27, Appli	Sequence 27, Appli
Sequence 28, Appli	Sequence 28, Appli
Sequence 29, Appli	Sequence 29, Appli
Sequence 30, Appli	Sequence 30, Appli
Sequence 31, Appli	Sequence 31, Appli
Sequence 32, Appli	Sequence 32, Appli
Sequence 33, Appli	Sequence 33, Appli
Sequence 34, Appli	Sequence 34, Appli
Sequence 35, Appli	Sequence 35, Appli
Sequence 36, Appli	Sequence 36, Appli
Sequence 37, Appli	Sequence 37, Appli
Sequence 38, Appli	Sequence 38, Appli
Sequence 39, Appli	Sequence 39, Appli
Sequence 40, Appli	Sequence 40, Appli
Sequence 41, Appli	Sequence 41, Appli
Sequence 42, Appli	Sequence 42, Appli
Sequence 43, Appli	Sequence 43, Appli
Sequence 44, Appli	Sequence 44, Appli
Sequence 45, Appli	Sequence 45, Appli
Sequence 46, Appli	Sequence 46, Appli
Sequence 47, Appli	Sequence 47, Appli
Sequence 48, Appli	Sequence 48, Appli
Sequence 49, Appli	Sequence 49, Appli
Sequence 50, Appli	Sequence 50, Appli
Sequence 51, Appli	Sequence 51, Appli
Sequence 52, Appli	Sequence 52, Appli
Sequence 53, Appli	Sequence 53, Appli
Sequence 54, Appli	Sequence 54, Appli
Sequence 55, Appli	Sequence 55, Appli
Sequence 56, Appli	Sequence 56, Appli
Sequence 57, Appli	Sequence 57, Appli
Sequence 58, Appli	Sequence 58, Appli
Sequence 59, Appli	Sequence 59, Appli
Sequence 60, Appli	Sequence 60, Appli
Sequence 61, Appli	Sequence 61, Appli
Sequence 62, Appli	Sequence 62, Appli
Sequence 63, Appli	Sequence 63, Appli
Sequence 64, Appli	Sequence 64, Appli
Sequence 65, Appli	Sequence 65, Appli
Sequence 66, Appli	Sequence 66, Appli
Sequence 67, Appli	Sequence 67, Appli
Sequence 68, Appli	Sequence 68, Appli
Sequence 69, Appli	Sequence 69, Appli
Sequence 70, Appli	Sequence 70, Appli
Sequence 71, Appli	Sequence 71, Appli
Sequence 72, Appli	Sequence 72, Appli
Sequence 73, Appli	Sequence 73, Appli
Sequence 74, Appli	Sequence 74, Appli
Sequence 75, Appli	Sequence 75, Appli
Sequence 76, Appli	Sequence 76, Appli
Sequence 77, Appli	Sequence 77, Appli
Sequence 78, Appli	Sequence 78, Appli
Sequence 79, Appli	Sequence 79, Appli
Sequence 80, Appli	Sequence 80, Appli
Sequence 81, Appli	Sequence 81, Appli
Sequence 82, Appli	Sequence 82, Appli
Sequence 83, Appli	Sequence 83, Appli
Sequence 84, Appli	Sequence 84, Appli
Sequence 85, Appli	Sequence 85, Appli
Sequence 86, Appli	Sequence 86, Appli
Sequence 87, Appli	Sequence 87, Appli
Sequence 88, Appli	Sequence 88, Appli
Sequence 89, Appli	Sequence 89, Appli
Sequence 90, Appli	Sequence 90, Appli
Sequence 91, Appli	Sequence 91, Appli
Sequence 92, Appli	Sequence 92, Appli
Sequence 93, Appli	Sequence 93, Appli
Sequence 94, Appli	Sequence 94, Appli
Sequence 95, Appli	Sequence 95, Appli
Sequence 96, Appli	Sequence 96, Appli
Sequence 97, Appli	Sequence 97, Appli
Sequence 98, Appli	Sequence 98, Appli
Sequence 99, Appli	Sequence 99, Appli
Sequence 100, Appli	Sequence 100, Appli

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

Om protein - protein search, using sw model

Run on: April 3, 2006, 08:22:56 ; Search time 176.536 Seconds
(without alignments)
2513.799 Million cell updates/sec

Title: US-10-715-667-21
Perfect score: 334

Sequence: 1 MNQVTLQWDAVIALVILFSW.TYFPQNILESHENRISLQE 629

Scoring table: BLOSUM62
Gappp 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : UniProt 05.80.*

1: uniprot_sprot;*
2: uniprot_trembl;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3334	100.0	629	2	Q5VWK5_HUMAN	Q5vwk5 homo sapien
2	3327	99.8	629	2	Q8NFQ9_HUMAN	Q8nfq9 homo sapien
3	3120	93.6	593	2	Q4VGP6_HUMAN	Q4vgp6 homo sapien
4	2282.5	68.5	644	2	Q8K4B4_MOUSE	Q8k4b4 mus musculus
5	1948	58.4	375	2	Q4VGP4_HUMAN	Q4vgp4 homo sapien
6	1895	56.8	390	2	Q5VWK7_HUMAN	Q5vwk7 homo sapien
7	1888	56.6	391	2	Q96AS1_HUMAN	Q96as1 homo sapien
8	1674	50.2	320	2	Q4VGP1_HUMAN	Q4vgp1 homo sapien
9	1655	49.6	320	2	Q4VGP3_HUMAN	Q4vgp3 homo sapien
10	1271	38.1	264	2	Q4VGP2_HUMAN	Q4vgp2 homo sapien
11	1175	35.2	227	2	Q8IW84_HUMAN	Q8iw84 homo sapien
12	705	21.1	138	2	Q4VGP5_HUMAN	Q4vgp5 homo sapien
13	335.5	10.1	869	2	Q5GR16_CHICK	Q5gr16 gallus gallus
14	281.5	8.4	918	2	Q9W6U9_CHICK	Q9w6u9 gallus gallus
15	277	8.3	554	2	Q8UAN2_TETNG	Q8uan2 tettigidea
16	261.5	7.8	917	1	Q16RB_MOUSE	Q16rb mus musculus
17	261.5	7.8	917	2	Q8PD19_MOUSE	Q8pd19 mus musculus
18	256.5	7.7	874	1	I12R2_MOUSE	I12r2 mus musculus
19	253.5	7.6	861	1	I12R2_BOVIN	I12r2 bovis
20	246.5	7.4	881	2	Q57515_XENLA	Q57515 xenopus laevis
21	245.5	7.4	1010	2	Q7TQ89_RAT	Q7tq89 rattus norvegicus
22	240.5	7.2	813	2	Q8UAN1_TETNG	Q8uan1 tettigidea
23	231.5	6.9	857	2	Q8FC04_HUMAN	Q8fc04 homo sapiens
24	230.0	6.9	918	1	I16RB_MOUSE	I16rb mus musculus
25	230.0	6.9	858	2	Q4QYCB_CANFA	Q4qycb canis familiaris
26	223	6.7	861	1	I12R2_PIG	I12r2 sus scrofa
27	222	6.7	862	1	I12R2_HUMAN	I12r2 homo sapiens
28	216	6.5	2030	2	Q8SE88_TETNG	Q8se88 tettigidea
29	215	6.5	918	1	I16RB_HUMAN	I16rb homo sapiens
30	215	6.1	622	2	Q5RAWO_PONPY	Q5rawo pongo pygmaeus
31	202					

32	198	5.9	617	2	Q75S21_RANCA	Q75s21 ranas catesbeiana
33	197.5	5.9	813	2	Q6DD37_XENLA	Q6dd37 xenopus laevis
34	195	5.8	764	2	Q6BBC3_HUMAN	Q6bbc3 homo sapiens
35	194	5.8	1097	1	Q1FLR_HUMAN	Q1flr homo sapiens
36	192	5.8	739	2	Q4T411_TETNG	Q4t411 tettigidea
37	191.5	5.7	649	2	Q6UAQ5_tetradon	Q6uaq5 tetraodon niger
38	187	5.6	662	2	Q6BBC3_HUMAN	Q6bbc3 homo sapiens
39	191.5	5.7	732	2	Q8N17_HUMAN	Q8n17 homo sapiens
40	191	5.7	622	1	PRLR_HUMAN	Prlr homo sapiens
41	189.5	5.7	870	2	Q6UANO_TETNG	Q6uano tettigidea
42	189	5.7	394	2	Q6UAQ5_TETNG	Q6uaq5 tettigidea
43	187	5.6	602	2	Q6UAQ2_BRARE	Q6uaq2 brachydanio rerio
44	186.5	5.6	581	1	PRLR_BOVIN	Prlr bovinus
45	186.5	5.6	422	1	Q510Y2_MOUSE	Q510y2 homo sapiens
46	186	5.6	1092	1	LIIFR_MOUSE	Liifr mus musculus
47	183.5	5.5	425	1	Q5F3Y5_CALJA	Q5f3y5 gallus gallus
48	183	5.5	389	2	Q6DG28_BRARE	Q6dg28 brachydanio rerio
49	178	5.3	1093	1	PRLR_CHICK	Prlr chick
50	177.5	5.3	49	1	Q96F35_HUMAN	Q96f35 homo sapiens
51	176.5	5.3	884	2	Q6UAM6_TEING	Q6uam6 tetradon niger
52	176.5	5.3	509	2	Q8WYJ5_HUMAN	Q8wyj5 homo sapiens
53	176.5	5.3	425	1	Q9Jm58_CALJA	Q9jm58 gallus gallus
54	170	5.1	609	2	Q5ISE1_CYPCA	Q5isel cyprinus carpio
55	166	5.0	601	2	Q6QDA0_CHICK	Q6qda0 gallus gallus
56	166	5.0	1093	1	Q9FTP0_CARAU	Q9ftp0 carassius auratus
57	165.5	5.0	422	1	Q6L1F7_EUBMA	Q6l1f7 eubranchus
58	164.5	4.9	604	2	Q6EBC5_HUMAN	Q6ebc5 homo sapiens
59	163	4.9	831	2	Q6LPR_RAT	Q6lpr rattus norvegicus
60	163	4.9	608	1	PRLR_SHEEP	Prlr ovis aries
61	163	4.9	1093	1	Q93404_OREMO	Q93404 oreocerophryslus
62	162.5	4.9	324	2	Q6EBC5_HUMAN	Q6ebc5 homo sapiens
63	161.5	4.8	600	2	Q6LPR_RAT	Q6lpr rattus norvegicus
64	161.5	4.8	830	2	Q6LPR_SHEEP	Q6lpr ovis aries
65	160.5	4.8	600	2	Q9FTP0_CARAU	Q9ftp0 carassius auratus
66	158	4.7	610	1	Q6LPR_RAT	Q6lpr rattus norvegicus
67	158	4.7	819	2	Q6LPR_SHEEP	Q6lpr ovis aries
68	157	4.7	610	1	Q6LPR_RAT	Q6lpr rattus norvegicus
69	157	4.7	819	2	Q6LPR_SHEEP	Q6lpr ovis aries
70	156.5	4.6	831	2	Q93404_OREMO	Q93404 oreocerophryslus
71	154.5	4.6	346	2	Q93404_OREMO	Q93404 oreocerophryslus
72	154.5	4.6	346	2	Q93404_OREMO	Q93404 oreocerophryslus
73	154.5	4.6	716	2	Q8R501_MOUSE	Q8r501 mus musculus
74	154	4.6	288	2	Q96P36_HUMAN	Q96p36 homo sapiens
75	154	4.6	492	2	Q6NZF0_MOUSE	Q6nzf0 mus musculus
76	154	4.6	603	2	Q9FTL_XENLA	Q9ftl xenopus laevis
77	154	4.6	616	1	PRLR_RABIT	Prlr rabbit
78	154	4.6	625	2	Q9XS92_TRIVU	Q9xs92 trichosurus vulpecula
79	153.5	4.6	547	2	Q6EAL7_MOUSE	Q6eal7 mus musculus
80	153.5	4.6	662	2	Q6EAL7_MOUSE	Q6eal7 mus musculus
81	153.5	4.6	716	2	Q8K5B1_MOUSE	Q8k5b1 mus musculus
82	153.5	4.6	831	1	PRLR_MELIGA	Prlr meligae
83	153.5	4.6	1165	1	Q8VH29_HUMAN	Q8vh29 trichosurus vulpecula
84	153	4.6	229	2	Q8VWK6_HUMAN	Q8vwk6 homo sapiens
85	153	4.6	1165	1	LPFR_HUMAN	Lpfr homo sapiens
86	152.5	4.6	611	2	Q9PTH9_XENLA	Q9pth9 xenopus laevis
87	151.5	4.5	1148	2	Q9IBA7_CHICK	Q9iba7 gallus gallus
88	151	4.5	581	1	PRLR_GERRL	Prlr gerbillus
89	151	4.5	608	1	PRLR_MOUSE	Prlr mus musculus
90	150.5	4.5	334	2	Q6UC85_CHICK	Q6uc85 gallus gallus
91	150.5	4.5	1148	2	Q9I1V6_GALL	Q9i1v6 gallus gallus
92	150.5	4.5	1166	2	Q4W810_CANFA	Q4w810 canis familiaris
93	149.5	4.5	557	2	Q5OEXB_SPARR	Q5oexb sparassus auratus
94	149.5	4.5	583	2	Q5OHO4_SPARR	Q5oh4 sparassus auratus
95	149.5	4.5	1128	2	Q5ZBC0_ORYSA	Q5zbc0 oryza sativa
96	149	4.5	608	1	Q99JZ1_MOUSE	Q99jz1 mus musculus
97	147.5	4.4	437	2	Q4RMP5_TETNG	Q4rmp5 tetradon niger
98	146.5	4.4	638	2	Q9DB08_ONCMY	Q9db08 oncomyces
99	145.5	4.4	1147	2	Q9DDK1_MELIGA	Q9ddk1 meligae
100	144.5	4.3	1165	2	Q5KQUS_BOVIN	Q5kqus bos taurinus

ALIGNMENTS

GenCore version 5.1.7
 Copyright (c) 1993 - 2006 Biocceleration Ltd.

Om protein - protein search, using bw model
 Run on: April 3, 2006, 08:24:45 ; Search time 26.5041 seconds
 (without alignments)
 1962.071 Million cell updates/sec

Title: US-10-715-667-21
 Perfect score: 3334
 Sequence: 1 MNQQTIQMDAVIALYIILFSW.....TYFPQNQILESHFNRISLLEK 629
 Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5
 Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060
 Minimum DB seq length: 0
 Maximum DB seq length: 2000000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 100 summaries

Database : Issued_Patents_A1:
 1: /cggn2_6/ptcdata1/iaa/5_COMB.pep: *
 2: /cggn2_6/ptcdata1/iaa/6_COMB.pep: *
 3: /cggn2_6/ptcdata1/iaa/H_COMB.pep: *
 4: /cggn2_6/ptcdata1/iaa/PCTUS_COMB.pep: *
 5: /cggn2_6/ptcdata1/iaa/RE_COMB.pep: *
 6: /cggn2_6/ptcdata1/iaa/Batchfile1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3314	99.4	629	2	US-09-853-180B-2	Sequence 2, Appli
2	232	7.0	951	2	US-09-313-94-9	Sequence 9, Appli
3	232	7.0	951	2	US-09-282-162-9	Sequence 9, Appli
4	222	6.7	862	1	US-08-685-118-2	Sequence 2, Appli
5	222	6.7	862	1	US-08-915-495-2	Sequence 2, Appli
6	222	6.7	862	1	US-08-914-520-2	Sequence 2, Appli
7	222	6.7	862	2	US-09-533-180B-4	Sequence 4, Appli
8	222	6.7	864	2	US-09-949-002-758	Sequence 7/58, Appli
9	220	6.6	859	2	US-10-282-162-7	Sequence 7, Appli
10	220	6.6	859	1	US-08-825-556-6	Sequence 6, Appli
11	217	6.5	918	2	US-09-312-611-6	Sequence 6, Appli
12	217	6.5	918	2	US-09-533-180B-3	Sequence 3, Appli
13	215	6.4	918	2	US-09-949-002-333	Sequence 333, Appli
14	215	6.4	918	2	US-09-949-002-333	Sequence 536, Appli
15	214	6.4	937	2	US-09-949-002-536	Sequence 10, Appli
16	213	6.4	332	2	US-09-313-942-10	Sequence 10, Appli
17	213	6.4	332	2	US-10-282-162-10	Sequence 4, Appli
18	213	6.4	658	1	US-08-825-556-8	Sequence 4, Appli
19	213	6.4	658	2	US-09-312-611-4	Sequence 4, Appli
20	212	6.4	708	1	US-07-797-556-2	Sequence 2, Appli
21	212	6.4	708	1	US-08-308-881-2	Sequence 2, Appli
22	212	6.4	708	1	US-09-058-263-2	Sequence 2, Appli
23	212	6.4	708	1	US-05-059-093-2	Sequence 2, Appli
24	212	6.4	708	2	US-09-058-264-2	Sequence 2, Appli
25	212	6.4	708	2	US-09-455-962-2	Sequence 2, Appli
26	212	6.4	708	4	PCT-US95-06530-2	Sequence 2, Appli
27	210	6.3	1158	2	US-09-313-942-26	Sequence 26, Appli

28	210	6.3	1158	2	US-10-282-162-26	Sequence 26, Appli
29	210	6.3	1168	2	US-09-313-942-24	Sequence 24, Appli
30	210	6.3	1168	2	US-10-282-162-24	Sequence 24, Appli
31	207.5	6.2	488	2	US-08-593-455-5	Sequence 5, Appli
32	207.5	6.2	488	2	US-09-063-781B-5	Sequence 5, Appli
33	207.5	6.2	488	2	US-09-137-132-5	Sequence 5, Appli
34	207.5	6.2	488	2	US-08-863-564A-5	Sequence 5, Appli
35	207.5	6.2	488	2	US-09-094-410-5	Sequence 5, Appli
36	207.5	6.2	488	2	US-08-788-123D-5	Sequence 5, Appli
37	207.5	6.2	488	2	US-08-583-153A-5	Sequence 5, Appli
38	207.5	6.2	488	2	US-08-638-524B-5	Sequence 5, Appli
39	194	5.8	1097	2	US-09-949-016-6209	Sequence 609, Appli
40	194	5.8	1097	1	US-09-949-016-10081	Sequence 1081, Appli
41	194	5.8	1001	1	US-07-943-843-2	Sequence 2, Appli
42	194	5.8	1097	1	US-07-943-843-6	Sequence 2, Appli
43	194	5.8	1097	1	US-08-317-003-6	Sequence 6, Appli
44	194	5.8	1097	1	US-09-949-016-6209	Sequence 6, Appli
45	194	5.8	1119	2	US-09-949-016-10081	Sequence 1081, Appli
46	194	5.8	1119	1	US-07-943-976-6	Sequence 6, Appli
47	191	5.7	637	2	US-09-949-016-10128	Sequence 10128, Appli
48	186.5	5.6	836	1	US-07-943-976-4	Sequence 1, Appli
49	186.5	5.6	836	1	US-07-943-976-2	Sequence 1, Appli
50	175.5	5.3	719	1	US-07-943-843-4	Sequence 1, Appli
51	176.5	5.3	719	1	US-08-317-003-4	Sequence 1, Appli
52	170	5.1	771	1	US-07-943-976-6	Sequence 6, Appli
53	170	5.1	783	6	52-224B-2	Sequence 6, Appli
54	170	5.1	836	1	US-07-943-976-4	Sequence 1, Appli
55	170	5.1	863	1	US-07-943-976-2	Sequence 1, Appli
56	167	5.0	572	1	US-08-419-632-5	Sequence 1, Appli
57	164.5	4.9	385	2	US-09-017-224-19	Sequence 1, Appli
58	164.5	4.9	405	2	US-09-017-224-2	Sequence 1, Appli
59	164.5	4.9	405	2	US-09-210-601-2	Sequence 2, Appli
60	164.5	4.9	425	2	US-09-011-224-6	Sequence 2, Appli
61	163.5	4.9	303	2	US-09-071-224-21	Sequence 2, Appli
62	163.5	4.9	389	2	US-09-071-224-24	Sequence 2, Appli
63	163.5	4.9	389	2	US-09-017-224-27	Sequence 2, Appli
64	163.5	4.9	389	2	US-09-017-224-29	Sequence 2, Appli
65	163.5	4.9	422	2	US-09-071-224-2	Sequence 2, Appli
66	162.5	4.9	303	2	US-09-017-224-23	Sequence 2, Appli
67	162.5	4.9	385	2	US-09-071-224-20	Sequence 2, Appli
68	162.5	4.9	388	2	US-09-071-224-17	Sequence 2, Appli
69	162.5	4.9	389	2	US-09-071-224-22	Sequence 2, Appli
70	162.5	4.9	389	2	US-09-071-224-26	Sequence 2, Appli
71	162.5	4.9	392	2	US-09-071-224-18	Sequence 2, Appli
72	162.5	4.9	410	2	US-09-531-355-12	Sequence 12, Appli
73	162.5	4.9	422	2	US-09-860-028-32	Sequence 32, Appli
74	162.5	4.9	422	2	US-09-944-457-32	Sequence 32, Appli
75	162.5	4.9	422	2	US-09-945-584-32	Sequence 32, Appli
76	162.5	4.9	422	2	US-09-944-943-32	Sequence 32, Appli
77	162.5	4.9	422	2	US-09-945-587-32	Sequence 32, Appli
78	162.5	4.9	425	2	US-09-071-224-4	Sequence 4, Appli
79	162.5	4.9	434	2	US-09-071-224-7	Sequence 4, Appli
80	162.5	4.9	434	2	US-09-120-601-4	Sequence 4, Appli
81	162.5	4.9	448	2	US-09-120-601-6	Sequence 6, Appli
82	161.5	4.8	349	2	US-08-860-597A-14	Sequence 14, Appli
83	161.5	4.8	349	2	US-08-770-428A-14	Sequence 14, Appli
84	161.5	4.8	389	2	US-09-071-224-28	Sequence 28, Appli
85	161.5	4.8	389	2	US-09-071-224-30	Sequence 30, Appli
86	160.5	4.8	389	2	US-09-071-224-31	Sequence 31, Appli
87	160.5	4.8	407	2	US-09-521-335-13	Sequence 13, Appli
88	159.5	4.8	389	2	US-09-071-224-25	Sequence 14, Appli
89	157	4.7	592	2	US-09-000-145-6	Sequence 6, Appli
90	156	4.6	1165	1	US-06-600-398A-11	Sequence 11, Appli
91	154	4.6	1165	1	US-09-000-145-4	Sequence 11, Appli
92	153	4.6	883	2	US-08-882-430-1	Sequence 13, Appli
93	153	4.6	1165	1	US-08-521-335-13	Sequence 13, Appli
94	153	4.6	1165	2	US-09-071-224-25	Sequence 14, Appli
95	153	4.6	1165	2	US-09-071-224-26	Sequence 14, Appli
96	153	4.6	1165	2	US-09-071-224-27	Sequence 14, Appli
97	153	4.6	1165	2	US-09-071-224-28	Sequence 14, Appli
98	153	4.6	1165	2	US-09-071-224-30	Sequence 14, Appli
99	153	4.6	1165	2	US-09-071-224-31	Sequence 14, Appli
100	153	4.6	1165	2	US-09-071-224-32	Sequence 14, Appli

ALIGNMENTS

RESULT 1
US-09-853-180B-2

; Patent No. 6756481
; GENERAL INFORMATION:

APPLICANT: Parham, Christi L.
APPLICANT: Kastlein, Robert A.

FILE REFERENCE: DX01074

SEARCHED SERIALIZED INDEXED OMB NO. 2552-0187
CURRENT FILING DATE: 2001-05-10
APPLICANT: RICHERON PHARMACEUTICALS, INC.

PRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 4
TITLE OF INVENTION: ...
FILED REFERENCE: REG 203-A

SOFTWARE: FastSEQ for Windows Version 3.1

NAME/KEY: misc feature
P-DATA-KEY: misc feature

US-09-853-180B-2
OTHER INFORMATION: Inc. Xaa. at location 126 stands for GRY, or AIG

Query Match Similarity Score 3314 / 99.4% Pred No 2.48-290: Rest Local

1. INNOVATION IN VENTURE CAPITAL FUNDING: THE CHINESE PERSPECTIVE 63

Db
1 MNKVTIOWDAVIALYLIFSWCHGGITNNINCSDHINVEPATIFKMGKHNISIYCOAIIKNCQ 60

121 SCYPPNT PDRUTCVT VEYSGNMTCITWNAGKET, TYITDTKVVWHSI RTTRECOYI TSSYT 180

Db 121 SGYPDPIDPEVTCVIYEYSGNMTCITWNAXKLTYIDTKYVWHVKSLETTEEBOQYLTSSYIN 180

卷之三

QY 241 YWDSOTTIEKVSCEMRYKATTNOTWNVKEPDTNFTTYVQOSEFYLEPNIKYVFQVRQCQBTG 300

DD 241 YWDSQITIEKVSCENRYKATIINOIWNKEFDINETYVQOQSEFYLEPNPKIVFQVRQENG 300

QY
361 IVEAVMLSLISLIGIFNRSFRTGKIRILLIPKWLVEDIPNMKNSNVYKMLQBNSELMN 420

卷之三

Db
421 NNSSEQVLYDPMMTBKEIPBHKPTDYKKENTGPLETRDYPPONSFLFDNT"VVYIPLD 4800

481 NTGYKPQISNFLPBPGBSHLSNNNEITSLLKPPVDSLDSGNPRLQKHPNFAFSVSVNSL 5400

GenCore version 5.1.7
 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using SW model

Run on: April 3, 2006, 08:22:41 ; Search time 60.2709 seconds
 (without alignments) 2595.264 Million cell updates/sec

Title: US-10-715-667-25
 Perfect score: 1934
 Sequence: 1 MNQVTTQMDAVIALVLFSW.....TVA SISTGHLTSGLKRGSYC 356

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext: 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
 Maximum DB seq length: 200000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 100 summaries

Database : A_Geneseq_21:*

- 1: geneseqD1980s:*
- 2: geneseqD1998s:*
- 3: geneseqD2008s:*
- 4: geneseqD2001s:*
- 5: geneseqD2002s:*
- 6: geneseqD2003s:*
- 7: geneseqD2005bs:*
- 8: geneseqD2008s:*
- 9: geneseqD2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1934	100.0	356	5 AAE24035
2	97.6	428	4 AAE24966	
3	97.6	629	4 AAB74967	
4	97.6	629	5 AAE24033	
5	97.3	384	4 AAB26564	
6	97.3	384	5 AAE24036	
7	97.3	384	7 ADC07177	
8	97.3	384	9 ADZ25012	
9	96.7	428	4 AAB24964	
10	96.7	629	4 AAB24965	
11	96.5	629	5 AAE24008	
12	96.6	629	8 ADT33605	
13	96.6	629	9 AEA1090	
14	89.6	565	5 AAE24034	
15	88.7	337	4 AAB24963	
16	147.5	73.3	644 5 AAE24038	
17	102.5	52.8	344 5 AAE24008	
18	261.5	13.5	917 2 AAR26334	
19	261.5	13.5	917 3 AY55073	
20	261.5	13.5	917 8 ADT66596	
21	230.5	11.9	918 7 ADE58225	
22	230.5	11.9	918 8 ADT66594	
23	227	11.7	861 5 ABB78098	
24	11.7		861 5 ABB78097	
25	222	11.5	862 2 AAW12771	
26	222	11.5	862 7 ADR39704	
27	222	11.5	862 7 ADFF6359	
28	222	11.5	862 8 ADK3069	
29	222	11.5	862 8 ADM33832	
30	222	11.5	862 8 ADL9580	
31	222	11.5	862 8 ADP34649	
32	222	11.5	862 9 ADY19580	
33	222	11.5	862 9 ADY15768	
34	222	11.5	862 9 AEA51092	
35	215.5	11.1	727 3 AAY92192	
36	215.5	11.1	738 3 AAY92194	
37	215.5	11.1	859 2 AAW0796	
38	215.5	11.1	859 3 AAY92184	
39	215.5	11.1	859 7 ABW02164	
40	215.5	11.1	951 2 AAW0798	
41	215.5	11.1	951 3 AAY92186	
42	215.5	11.1	951 7 ABW02166	
43	215.5	11.1	961 3 AAY92197	
44	213	11.0	332 2 AAW0799	
45	213	11.0	332 3 AAY92118	
46	213	11.0	332 7 ABW02167	
47	212.5	11.0	658 2 AAR94576	
48	212.5	11.0	918 2 AAR10545	
49	212.5	11.0	918 2 AAR6233	
50	212.5	11.0	918 2 AAR75368	
51	212.5	11.0	918 3 AAY4644	
52	212.5	11.0	918 5 ABP05551	
53	212.5	11.0	918 6 ABR47497	
54	212.5	11.0	918 7 ADE58227	
55	212.5	11.0	918 7 ADF17837	
56	212.5	11.0	918 7 ADN38756	
57	212.5	11.0	918 8 ADP66592	
58	212.5	11.0	918 9 AEA51091	
59	211.5	10.9	708 2 AAB85911	
60	211.5	10.9	918 7 ADY15450	
61	211.5	10.9	918 9 ADY16528	
62	211.5	10.9	918 9 ADY16723	
63	208	10.8	326 5 ADM1264	
64	208	10.8	329 2 AAW17859	
65	208	10.8	329 8 ADR14425	
66	207.5	10.7	488 4 AAE12610	
67	207.5	10.7	488 8 ADG62980	
68	207.5	10.7	488 8 ADG62980	
69	207.5	10.7	809 5 AAY75499	
70	207.5	10.7	158 3 AAY92205	
71	207.5	10.7	158 7 ABW02178	
72	207.5	10.7	168 3 AAY92204	
73	207.5	10.7	168 3 AY92204	
74	207	10.7	329 9 ADY15432	
75	199.5	10.3	708 2 AAR37804	
76	196.1	10.1	36 4 ABB32440	
77	186.5	9.6	837 8 ADP59673	
78	186.5	9.6	837 9 ABB1063	
79	182.5	9.4	837 4 ABB1254	
80	182	9.4	1001 2 AAR37806	
81	182	9.4	1097 2 AAR45776	
82	182	9.4	1097 2 AAR74097	
83	182	9.4	1097 8 ABB04595	
84	182	9.4	1097 8 ABB04595	
85	182	9.4	1522 2 AAR70125	
86	182	9.4	1522 2 AAR70125	
87	181	9.4	1001 2 AAR45774	
88	180	9.3	334 2 AAR99140	
89	177.5	9.2	1001 2 AAR74095	
90	177	9.2	1001 2 AAR74095	
91	174	9.0	1001 2 AAR49506	
92	172.5	8.9	984 2 ABB8686	
93	170	8.8	771 2 AAR14255	
94	170	8.8	783 2 AAR17141	
95	170	8.8	783 2 AAR17868	
96	170	8.8	783 2 AAW10486	
97	170	8.8	AAW10486	

Aaw12771 Human int
 Ad319704 Human int
 Adf6359 Novel hum
 Adk3069 Human IL-
 Adm33832 Human IL-
 Adl9580 Human PRO
 Adg54649 Human PRO
 Ady19580 PRO polyp
 Ady15768 PRO polyp
 Aea51092 Human IL-
 Aav92186 Human gpl
 Abw02166 Human gpl
 Aav92187 Human gpl
 Aav92188 Human gpl
 Aav92189 Human gpl
 Abw02167 Human gpl
 Abx05551 Breast ca
 Abx94576 Human gpl
 Aax12610 Human PRO
 Aax46233 Human sol
 Aax75368 Human gpl
 Aav4644 Human gpl
 Abx16723 PRO polyp
 Aav16723 PRO polyp
 Aav1264 Human gpl
 Aav17859 Rheumatol
 Adr14425 Human NF-
 Aae12610 Human gpl
 Aae23860 Human Ob
 Adg62980 Human gpl
 Aau75498 Human int
 Aav92205 Fusion po
 Abw02178 Human cyt
 Aav92204 Fusion po
 Abw02177 Human cyt
 Ady15432 PRO polyp
 Aax37804 Human gpl
 Abx32440 Peptide #
 Adg59673 Murine GC
 Abi1063 Murine G-C
 Abi14254 Murine GC
 Aar14254 Murine GC
 Aar37806 Human LIF
 Aar45774 Human leu
 Aar4908 Human LIF
 Aar45776 Human leu
 Aar74097 Human leu
 Aar84695 Human can
 Abp12320 Human LIF
 Aar70125 LIF-R-GBP
 Aar86868 TIGI PC r
 Aar14255 Human GCS
 Aar11741 Granulocy
 Aar77868 Human pla
 Aav10485 Human gra
 Aaw10486 Human gra

98 170 8.8 801 2 ARI1742
 99 170 8.8 814 4 ARI30059
 100 170 8.8 824 4 ARI23678

ALIGNMENTS

RESULT 1

AAE24035 standard; protein; 356 AA.

AAE24035;

XX 23-SEP-2002 (first entry)

XX DE Human haematopoietin receptor .2 (HPR2) ex9 protein.

XX Human; haematopoietin receptor; receptor; HPR1; HPR2; cell proliferation;

XX pancytopenia; leukaemia; anaemia; thrombocytopaenia; osteoporosis;

XX neurodegenerative disorder; leukaemia; carcinoma; haematologic disorder;

XX cancer; myelodysplastic syndrome; idiopathic thrombocytopaenic purpura;

XX ITP; sickle cell vasoocclusive crisis; myelofibrosis; myeloid metaplasia;

XX osteoclast disorder; periodontitis; acute polyneuropathy; Bell's Palsy;

XX anorexia nervosa; chronic fatigue syndrome; Guillain-Barre syndrome; Guillain-Barre syndrome; vertebral disc disease; myasthenia gravis; chronic neuronal degeneration;

XX vertebral disc disease; myasthenia gravis; chronic neuronal degeneration;

XX stroke; fatigue; tumour; sarcoma; osteoporosis; obesity; infertility;

XX ischaemic disease.

XX Homo sapiens.

XX WO200229060-A2.

XX PD 11-APR-2002.

XX 05-OCT-2001; 2001WO-US031634.

XX PR 06-OCT-2000; 2000US-0238706P.

XX PR 13-OCT-2000; 2000US-024076P.

XX PR 20-FEB-2001; 2001US-0270282P.

XX (IMMV) IMMUNEX CORP.

XX PI Cosman DJ, Mosley BA, Bird TA, Dubose RF, Wiley SR;

XX DR WPI; 2002-330172/36.

XX DR N-PSB; ARI38775.

XX PT Human and murine hematopoietin receptor polypeptides HPR1 and HPR2, useful for treating cell proliferation, metabolic, and reproductive hormone related conditions.

XX PS Claim 3; Page 127-129; 136pp; English.

XX The present invention relates to human and murine haematopoietin receptor polypeptides HPR1 and HPR2. Sequences of the invention are useful for treating cell proliferation conditions e.g., pancytopenia, leukaemia, anaemia, thrombocytopaenia, neurodegenerative disorders and osteoporosis resulting from a lack of bone-forming cells. They are also useful for treating cell proliferation conditions such as leukaemia and tumour metastasis, osteoporosis resulting from an excess of bone-resorbing cells. HPR sequences are also useful for treating medical conditions and diseases such as cell proliferation, metabolic and reproductive hormone related conditions. They are useful for treating various hematologic and oncologic disorders e.g., Epstein-Barr virus-positive nasopharyngeal carcinoma, myelogenous leukaemia, colon, stomach, prostate, renal cell, cervical and ovarian cancers, lung cancer (SCC and NSCC), including cancer-associated cachexia, fatigue, solid tumours (e.g., osteosarcoma, sarcoma), carcinoma (e.g., adenocarcinoma (for example, breast cancer), squamous cell carcinoma), haematologic disorders, anaemia (e.g., anaemia, dysplastic syndrome (including refractory anaemia, refractory anaemia,

Arar1742 Clone 25-Aau30059 Novel human Ram23678 Human EST

CC with ringed sideroblasts or with excess blasts), idiopathic thrombocytopaenic purpura (ITP), sickle cell vasoocclusive crisis, myelofibrosis/osteoporosis including post-menopausal osteoporosis, periodontitis resulting in tooth loosening or loss, prosthesis loosening after joint replacement, neurodegenerative conditions (e.g., acute polyneuropathy, Bell's palsy, anorexia nervosa, chronic fatigue syndrome, transmissible dementia including Creutzfeld-Jacob disease, demyelinating neuropathy, Guillain-Barre syndrome, vertebral disc disease, Gulf war syndrome, myasthenia gravis, chronic neuronal degeneration, stroke including cerebral ischaemic diseases. HPR1 and HPR2 polypeptides are also useful for treating various other disorders such as osteoporosis, obesity, deficient mammary development and infertility. The present sequence is human HPR2 ex9 protein

XX SQ Sequence 356 AA;

Query Match 100.0%; Score 1934; DB 5; Length 356;
 Best Local Similarity 100.0%; Pred. No. 4.1e-162; Matches 356; Conservative 0; Mismatches 0; Gaps 0;

QY 1 MNQVITQWDAVIALYVILFSNCHGGTNTNGNSHINWEPATIFKQGMNISIYQQAIIKNCQ 60
 Db 1 MNQVITQWDAVIALYVILFSNCHGGTNTNGNSHINWEPATIFKQGMNISIYQQAIIKNCQ 60

QY 61 PRKLHRYKNGTKERFOITRINKTARLWYKPLPHASMYCTAECPKHFOSTLGGDIS 120
 Db 61 PRKLHRYKNGTKERFOITRINKTARLWYKPLPHASMYCTAECPKHFOSTLGGDIS 120

QY 121 SGYPPDIPDDEUTCVIYEYSQMTCTNAGKLTIDTKYVWHVSKLRTBESQYLSSYYIN 180
 Db 121 SGYPPDIPDDEUTCVIYEYSQMTCTNAGKLTIDTKYVWHVSKLRTBESQYLSSYYIN 180

QY 181 ISTDSIQQGGKELVWQVANALGMEKRSKQLOIHLDDITVSAVTSRAETINATPTII 240
 Db 181 ISTDSIQQGGKELVWQVANALGMEKRSKQLOIHLDDITVSAVTSRAETINATPTII 240

QY 241 YMDSQTTIEKVSCEMYKATTNQTVKEFDNTFVQOQSFYLEPNKIVFQVRQCBTG 300
 Db 241 YMDSQTTIEKVSCEMYKATTNQTVKEFDNTFVQOQSFYLEPNKIVFQVRQCBTG 300

QY 301 KRYWQWSSLFLPKHPTPTVPOVTSKAFQHDNTNSGIVTAISTGHLSGLKRGSYC 356
 Db 301 KRYWQWSSLFLPKHPTPTVPOVTSKAFQHDNTNSGIVTAISTGHLSGLKRGSYC 356

SQ

RESULT 2

ID AAB74966

ID AAB74966;

AC AAB74966;

DT 11-JUL-2001 (first entry)

XX DE Human haemopoietin receptor protein NR12.4 SEQ ID NO:8

XX Human; haemopoietin receptor protein; NR12; immunosuppressive;

XX antiallergic; haemopoietin factor; autoimmune disease; tissue rejection;

XX metal allergy; pollen allergy.

XX Homo sapiens.

XX WO200123556-A1.

XX PD 05-APR-2001.

XX 27-SEP-2000; 2000WO-JP006654.

XX PR 27-SEP-1999; 99JP-00273358.

XX PR 03-AUG-2000; 2000JP-00240397.

XX PA (CHUG-) CHUGAI RRS INST MOLECULAR MEDICINE INC.

XX

GenCore version 5.1.7	32	18.5	9.6	837	1	CSP3R MOUSE
Copyright (c) 1993 - 2006 Biocceleration Ltd.	33	18.6	9.6	477	2	Q5F3Y5 CHICK
Run on: April 3, 2006, 08:22:56 ; Search time 99.9157 Seconds	34	18.2	9.4	1097	1	LIFR_HUMAN
(without alignments) 2513.799 Million cell updates/sec	35	17.8.5	9.2	870	2	Q5UANO_TETNG
Scoring table: BLOSUM62	36	17.8.5	9.2	175	2	Q5SS21_PANCA
Searched: Gapop 10.0 , Gapext 0.5	37	17.5	9.0	389	2	Q5DQ28_BRARE
Total number of hits satisfying chosen parameters: 216643	38	17.2	8.9	389	2	Q5TB3R_HUMAN
Minimum DB seq length: 0	39	17.0	8.8	836	1	Q5J0T2_MOUSE
Maximum DB seq length: 200000000	40	16.8	8.7	719	2	LIFR_MOUSE
Database : UniProt 05.80;*	41	16.7	8.7	1092	1	CRFL1_MOUSE
1: uniprot_sprot;*	42	16.7	8.6	425	1	CRFL1_HUMAN
2: uniprot_trembl;*	43	16.2.5	8.4	422	1	Q5DQ28_BRARE
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	44	16.1.5	8.4	50	2	Q5TB3R_HUMAN
Post-processing: Minimum Match 0% Maximum Match 100%	45	15.1.5	8.4	1093	2	Q5TB35_RAT
Listing first 100 summaries	46	15.1	8.3	52	2	Q516F7_EUBOMA
SUMMARIES	47	15.8	8.2	819	2	Q5WV6K_HUMAN
1: UniProt 05.80;*	48	15.8	8.2	509	2	Q5WVJ0_HUMAN
2: uniprot_sprot;*	49	15.8	8.2	649	2	Q5BEC6_HUMAN
3: uniprot_trembl;*	50	15.8	8.2	662	2	Q5BEC3_HUMAN
4: uniprot_sprot;*	51	15.8	8.2	732	2	Q5WV17_HUMAN
5: uniprot_trembl;*	52	15.8	8.2	1093	2	Q5TB35_RAT
6: uniprot_sprot;*	53	15.3	7.9	229	2	Q5WVJ0_HUMAN
7: uniprot_trembl;*	54	15.1.5	7.8	547	2	Q5BEC6_MOUSE
8: uniprot_sprot;*	55	15.1.5	7.8	62	2	Q5BEC6_MOUSE
9: uniprot_trembl;*	56	15.1.5	7.8	716	2	Q5BEC3_HUMAN
10: uniprot_sprot;*	57	15.1.5	7.8	2	Q5WV51_MOUSE	
11: uniprot_trembl;*	58	15.1.5	7.8	1148	2	Q5TB17_CHICK
12: uniprot_sprot;*	59	15.0.5	7.8	334	2	Q5UC85_CHICK
13: uniprot_trembl;*	60	15.0.5	7.8	492	2	Q5WZF0_MOUSE
14: uniprot_sprot;*	61	15.0.5	7.8	1148	2	Q5TB18_CHICK
15: uniprot_trembl;*	62	15.0	7.8	622	2	Q5B5V4_MOUSE
16: uniprot_sprot;*	63	14.7	7.6	288	2	Q5B6P36_HUMAN
17: uniprot_trembl;*	64	14.7	7.6	349	2	Q5WVJ5_HUMAN
18: uniprot_sprot;*	65	14.7	7.6	376	2	Q5B6P35_HUMAN
19: uniprot_trembl;*	66	14.7	7.6	581	1	PRUR_BOVIN
20: uniprot_sprot;*	67	14.7	7.6	622	1	PRUR_HUMAN
21: uniprot_trembl;*	68	14.7	7.6	622	2	Q5RAWO_PONY
22: uniprot_sprot;*	69	14.6.5	7.6	437	2	Q5RMP5_TETNG
23: uniprot_trembl;*	70	14.6.5	7.6	604	2	Q5OGCS4_CYPICA
24: uniprot_sprot;*	71	14.5	7.5	1147	1	Q5DQK1_MELGKA
25: uniprot_trembl;*	72	14.3	7.4	581	1	PRUR_SHEEP
26: uniprot_sprot;*	73	14.2.5	7.4	602	2	Q5B22_BRARE
27: uniprot_trembl;*	74	14.2	7.4	600	2	Q5RMP0_CARAU
28: uniprot_sprot;*	75	14.1.5	7.3	622	2	Q5R0J7_CALJA
29: uniprot_trembl;*	76	14.1.5	7.3	1	PRUR_CHICK	
30: uniprot_sprot;*	77	14.1.5	7.3	831	1	Q5DPA0_CHICK
31: uniprot_trembl;*	78	14.0.5	7.3	460	2	Q5T2Z0_CHICK
32: uniprot_sprot;*	79	14.0	7.2	268	2	Q5TB78_HUMAN
33: uniprot_trembl;*	80	13.9.5	7.2	609	2	Q5ISEI_CYPICA
34: uniprot_sprot;*	81	13.8.5	7.2	623	1	Q5TRA_MOUSE
35: uniprot_trembl;*	82	13.6	7.0	360	2	Q5QAP0_TETNG
36: uniprot_sprot;*	83	13.6	7.0	818	2	Q5D4Q2_MOUSE
37: uniprot_trembl;*	84	13.6	7.0	1162	1	LBPR_MOUSE
38: uniprot_sprot;*	85	13.6	7.0	1165	1	LBPR_PIG
39: uniprot_trembl;*	86	13.6	7.0	1166	1	Q5W810_CANFA
40: uniprot_sprot;*	87	13.3	6.9	659	2	Q5G138_HUMAN
41: uniprot_trembl;*	88	13.2.5	6.9	346	2	Q53404_OREMO
42: uniprot_sprot;*	89	13.2	6.8	881	2	Q54222_NYOLU
43: uniprot_trembl;*	90	13.2	6.8	1153	2	Q5XXB8_MYTOLU
44: uniprot_sprot;*	91	13.1.5	6.8	831	1	P48356_mus_musculus
45: uniprot_trembl;*	92	13.1	6.8	1165	1	P48357_sus_scrofa
46: uniprot_sprot;*	93	13.0	6.7	283	2	Q5UCB4_CHICK
47: uniprot_trembl;*	94	13.0	6.7	581	1	P41910_CEREBEL
48: uniprot_sprot;*	95	13.0	6.7	1162	1	LBPR_RAT
49: uniprot_trembl;*	96	12.9.5	6.7	894	2	Q5UW77_TETNG
50: uniprot_sprot;*	97	12.7.5	6.7	227	2	Q5QW33_URSMA
51: uniprot_trembl;*	98	12.6.5	6.5	830	1	P41910_CEREBEL
52: uniprot_sprot;*	99	12.6.5	6.5	1083	2	Q5QFO7_CHICK
53: uniprot_trembl;*	100	12.5.5	6.5	310	2	Q58DZ7_RAT

ALIGNMENTS

Copyright (c) 1993 - 2006 Biocceleration Ltd.	32	18.5	9.6	837	1	P40223_mus_musculus
Run on: April 3, 2006, 08:22:56 ; Search time 99.9157 Seconds	33	18.6	9.6	477	2	Q5F3Y5_gallus_gallus
(without alignments) 2513.799 Million cell updates/sec	34	18.2	9.4	1097	1	P42702_homo_sapiens
Scoring table: Gapop 10.0 , Gapext 0.5	35	17.8.5	9.2	870	2	Q4t141_tetradon_nigrovittatum
Searched: 216643 seqs, 705528306 residues	36	17.8.5	9.2	175	2	Q5UANO_TETNG
Total number of hits satisfying chosen parameters: 216643	37	17.5	9.0	389	2	Q5SS21_PANCA
Minimum DB seq length: 0	38	17.2	8.9	389	2	Q5DQ28_BRARE
Maximum DB seq length: 200000000	39	17.0	8.8	836	1	Q5P3R_HUMAN
Database : UniProt 05.80;*	40	16.8	8.7	719	2	Q5J0T2_MOUSE
1: uniprot_sprot;*	41	16.8	8.7	1092	1	LIFR_MOUSE
2: uniprot_trembl;*	42	16.7	8.6	425	1	CRFL1_MOUSE
3: uniprot_sprot;*	43	16.2.5	8.4	422	1	CRFL1_HUMAN
4: uniprot_trembl;*	44	16.1.5	8.4	50	2	Q5DQ28_BRARE
5: uniprot_sprot;*	45	15.1.5	8.4	1093	2	Q5TB35_RAT
6: uniprot_trembl;*	46	15.1	8.3	52	2	Q516F7_EUBOMA
7: uniprot_sprot;*	47	15.8	8.2	819	2	Q5WV6K_HUMAN
8: uniprot_trembl;*	48	15.8	8.2	229	2	Q5WVJ0_HUMAN
9: uniprot_sprot;*	49	15.8	8.2	649	2	Q5BEC6_HUMAN
10: uniprot_trembl;*	50	15.8	8.2	662	2	Q5BEC3_HUMAN
11: uniprot_sprot;*	51	15.8	8.2	732	2	Q5WV17_HUMAN
12: uniprot_trembl;*	52	15.8	8.2	1093	2	Q5TB35_RAT
13: uniprot_sprot;*	53	15.3	7.9	229	2	Q5J0T2_MOUSE
14: uniprot_trembl;*	54	15.1.5	7.8	227	2	Q5DQ28_BRARE
15: uniprot_sprot;*	55	15.1.5	7.8	1148	2	Q5TB17_CHICK
16: uniprot_trembl;*	56	15.1.5	7.8	622	2	Q5B5V4_MOUSE
17: uniprot_sprot;*	57	15.0.5	7.8	288	2	Q5B6P36_HUMAN
18: uniprot_trembl;*	58	15.0.5	7.8	349	2	Q5WVJ5_HUMAN
19: uniprot_sprot;*	59	14.7	7.6	376	2	Q5B6P35_HUMAN
20: uniprot_trembl;*	60	14.7	7.6	581	1	PRUR_BOVIN
21: uniprot_sprot;*	61	14.7	7.6	622	1	PRUR_HUMAN
22: uniprot_trembl;*	62	14.7	7.6	622	2	Q5RAWO_PONY
23: uniprot_sprot;*	63	14.6.5	7.6	437	2	Q5RMP5_TETNG
24: uniprot_trembl;*	64	14.6	7.6	604	2	Q5OGCS4_CYPICA
25: uniprot_sprot;*	65	14.5	7.5	1147	1	Q5DQK1_MELGKA
26: uniprot_trembl;*	66	14.3	7.4	581	1	PRUR_SHEEP
27: uniprot_sprot;*	67	14.2.5	7.4	602	2	Q5B22_BRARE
28: uniprot_trembl;*	68	14.2	7.3	600	2	Q5RMP0_CARAU
29: uniprot_sprot;*	69	14.1.5	7.3	622	2	Q5R0J7_CALJA
30: uniprot_trembl;*	70	14.1.5	7.3	1	PRUR_CHICK	
31: uniprot_sprot;*	71	14.1.5	7.3	831	1	Q5DPA0_CHICK
32: uniprot_trembl;*	72	14.0.5	7.3	460	2	Q5T2Z0_CHICK
33: uniprot_sprot;*	73	14.0	7.2	268	2	Q5TB78_HUMAN
34: uniprot_trembl;*	74	14.0	7.2	609	2	Q5ISEI_CYPICA
35: uniprot_sprot;*	75	14.1.5	7.3	623	1	Q5TRA_MOUSE
36: uniprot_trembl;*	76	14.1.5	7.3	360	2	Q5QAP0_TETNG
37: uniprot_sprot;*	77	14.1.5	7.3	818	2	Q5D4Q2_MOUSE
38: uniprot_trembl;*	78	14.0.5	7.3	1162	1	LBPR_MOUSE
39: uniprot_sprot;*	79	14.0	7.2	1165	1	LBPR_PIG
40: uniprot_trembl;*	80	13.9.5	7.2	609	2	Q5W810_CANFA
41: uniprot_sprot;*	81	13.8.5	7.2	623	1	Q5G138_HUMAN
42: uniprot_trembl;*	82	13.6	7.0	360	2	Q5QAP0_TETNG
43: uniprot_sprot;*	83	13.6	7.0	818	2	Q5D4Q2_MOUSE
44: uniprot_trembl;*	84	13.6	7.0	1162	1	LBPR_MOUSE
45: uniprot_sprot;*	85	13.6	7.0	1165	1	LBPR_PIG
46: uniprot_trembl;*	86	13.6	7.0	1166	1	Q5W810_CANFA
47: uniprot_sprot;*	87	13.3	6.9	659	2	Q5G138_HUMAN
48: uniprot_trembl;*	88	13.2.5	6.9	346	2	Q53404_OREMO
49: uniprot_sprot;*	89	13.2	6.8	881	2	Q54222_NYOLU
50: uniprot_trembl;*	90	13.2	6.8	1153	2	Q5XXB8_MYTOLU
51: uniprot_sprot;*	91	13.1.5	6.8	831	1	P48356_mus_musculus
52: uniprot_trembl;*	92	13.1	6.8	1165	1	P48357_sus_scrofa
53: uniprot_sprot;*	93	13.0	6.7	283	2	Q5UCB4_CHICK
54: uniprot_trembl;*	94	13.0	6.7	581	1	P41910_CEREBEL
55: uniprot_sprot;*	95	13.0	6.7	1162	1	LBPR_RAT
56: uniprot_trembl;*	96	12.9.5	6.7	894	2	Q5UW77_TETNG
57: uniprot_sprot;*	97	12.7.5	6.7	227	2	Q5QW33_URSMA
58: uniprot_trembl;*	98	12.6.5	6.5	830	1	P41910_CEREBEL
59: uniprot_sprot;*	99	12.6.5	6.5	1083	2	Q5QFO7_CHICK
60: uniprot_trembl;*	100	12.5.5	6.5	310	2	Q58DZ7_RAT

RESULT 1
 OSWIK5 HUMAN
 ID OSWIK5; HUMAN PRELIMINARY; PRT; 629 AA.
 AC
 OSWIK5;
 AC
 OSWIK5; HUMAN PRELIMINARY; PRT; 629 AA.
 DT 01-FEB-2005 (TREMBrel. 29, last sequence update)
 DT 13-SEP-2005 (TREMBrel. 31, Last annotation update)
 DB Interleukin-23 receptor.
 GN Name=IL23R; OPENNames=RP1-131Q15.1-001;
 OS Homo sapiens (Human);
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1];
 RN NUCLOBOTIDE SEQUENCE.
 RP MEDLINE-22018152; PubMed=12023369;
 RX Parham C., Chilica M., Timans J., Vaiberg E., Travis M., Cheung J.,
 RA Pflanz S., Zhang R., Singh K.P., Vega F., To W., Wagner J.,
 RA Rennick D.M., Kastlein R.A., de Waal Malefyt R., Moore K.W.,
 RA O'Farrell A.-M., McClanahan T., Zurawski S., Hannum C., Gorman D.,
 RA J. Immunol. 168: 5699-5708 (2002).
 RL 12Rbeta1 and a novel cytokine receptor subunit, IL-23R.;"
 RL DR EMBL; ALJ89925; CAH70406; 1; -; Genomic DNA.
 DR Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; ALJ09843; CAH70406; 1; -; Genomic DNA.
 DR EMBL; ALJ09843; CAH70406; 1; JOINED; Genomic DNA.
 DR HGNC: HGNC:19100; IL23R.
 DR HGNC: HGNC:19100; IL23R.
 DR PROSITE; PS5053; FN3; 2.
 KW Receptor; Repeat; Transmembrane.
 SQ SEQUENCE 629 AA; 71722 MW; AC63C8981AABP05 CRC64;
 Query Match 97.6%; Score 1888; DB 2; Length 629;
 Best Local Similarity 100.0%; Pred. No. 7.4e-141;
 Matches 348; Conservative 0; Mismatches 0; Gaps 0;
 QY 1 MNQVITQWDAVIALYILPSWCHGGITNINGSGHINWEPATIFKGMNISTYQQAIRNQ 60
 Db 1 MNQVITQWDAVIALYILPSWCHGGITNINGSGHINWEPATIFKGMNISTYQQAIRNQ 60
 Db PRKLHFKYKNGIKERFOITRINKTARLWYKPNPLERHASMYCTAECPKHFOETLICGKDIS 120
 QY 61 PRKLHFKYKNGIKERFOITRINKTARLWYKPNPLERHASMYCTAECPKHFOETLICGKDIS 120
 Db 61 PRKLHFKYKNGIKERFOITRINKTARLWYKPNPLERHASMYCTAECPKHFOETLICGKDIS 120
 QY 121 SGYPPDIPDEVTCVYIEYSGNMTCTWAGKLTIDTKYVHVKSLTEBHQYLTSYIN 180
 Db 121 SGYPPDIPDEVTCVYIEYSGNMTCTWAGKLTIDTKYVHVKSLTEBHQYLTSYIN 180
 Db PRKLHFKYKNGIKERFOITRINKTARLWYKPNPLERHASMYCTAECPKHFOETLICGKDIS 120
 QY 181 ISTSLQGKXLYLWVQANALGMEESKQLOQIHDIVIPSAAVISRASFTINATPKTII 240
 Db 181 ISTSLQGKXLYLWVQANALGMEESKQLOQIHDIVIPSAAVISRASFTINATPKTII 240
 QY 241 YMDQTTIEKVSCEMRYKATTNQTVNKERDTNFTIVQOSEFVYEPNIKVFOVRQCGTG 300
 Db 241 YMDQTTIEKVSCEMRYKATTNQTVNKERDTNFTIVQOSEFVYEPNIKVFOVRQCGTG 300
 Db 181 ISTSLQGKXLYLWVQANALGMEESKQLOQIHDIVIPSAAVISRASFTINATPKTII 240
 QY 301 KRYWQWSSLPFKTPETPVQVTSKAFQHDITWNSGLTVASISTGHTS 348
 Db 301 KRYWQWSSLPFKTPETPVQVTSKAFQHDITWNSGLTVASISTGHTS 348
 RESULT 2
 Q8NFG9 HUMAN
 ID Q8NFG9_HUMAN PRELIMINARY; PRT; 629 AA.
 AC
 Q8NFG9;
 AC
 Q8NFG9; HUMAN PRELIMINARY; PRT; 629 AA.
 DT 01-OCT-2002 (TREMBrel. 22, Created)
 DT 01-OCT-2002 (TREMBrel. 22, Last sequence update)
 DT 01-MAR-2004 (TREMBrel. 26, Last annotation update)
 DE Interleukin-23 receptor.

RESULT 2
 Q8NFG9 HUMAN
 ID Q8NFG9_HUMAN PRELIMINARY; PRT; 629 AA.
 AC
 Q8NFG9;
 AC
 Q8NFG9; HUMAN PRELIMINARY; PRT; 629 AA.
 DT 01-OCT-2002 (TREMBrel. 22, Created)
 DT 01-OCT-2002 (TREMBrel. 22, Last sequence update)
 DT 01-MAR-2004 (TREMBrel. 26, Last annotation update)
 DE Interleukin-23 receptor.

RESULT 3
 Q4VGP1 HUMAN
 ID Q4VGP1_HUMAN PRELIMINARY; PRT; 320 AA.
 AC Q4VGP1;
 AC
 DT 13-SEP-2005 (TREMBrel. 31, Created)
 DT 13-SEP-2005 (TREMBrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBrel. 31, Last annotation update)
 DE Interleukin-23 receptor isoform 4 (Fragment).
 OS Homo sapiens (Human).
 OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1];
 RN NUCLOBOTIDE SEQUENCE.
 RA Zhang X.-Y., Zhang Y., Zhang H.-J., Wang S.-H., Liu L.,

Copyright (c) 1993 - 2006 Biocceleration Ltd.	GenCore version 5.1.7			
Run on: April 3, 2006, 08:24:45 ; Search time 15.0008 Seconds	(without alignments)			
Scoring table: BLOSUM62	1962.071 Million cell updates/sec			
Searched: 572060 seqs, 82675679 residues				
Post-processing: Minimum Match 0%				
Minimum DB seq length: 0				
Maximum DB seq length: 200000000				
Database : Issued_Patents_AA:*				
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*				
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*				
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*				
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*				
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*				
6: /cgn2_6/ptodata/1/iaa/bacfiles1.pep:*				
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.				
SUMMARIES				
Result No.	Score	Query Match Length	DB ID	Description
1	1868	96.6	629	2 US-09-853-180B-2
2	222	11.5	862	1 US-08-655-182
3	222	11.5	862	1 US-08-915-493-2
4	222	11.5	862	1 US-08-914-520-2
5	222	11.5	862	2 US-09-853-180B-4
6	222	11.5	864	2 US-09-910-7758
7	215.5	11.1	859	2 US-09-313-942-7
8	215.5	11.1	859	2 US-09-202-162-7
9	215.5	11.1	951	2 US-09-313-942-9
10	215.5	11.1	951	2 US-10-202-162-9
11	213	11.0	332	2 US-09-313-942-10
12	213	11.0	332	2 US-10-202-162-10
13	212.5	11.0	658	1 US-08-825-558-4
14	212.5	11.0	658	2 US-09-312-611-4
15	212.5	11.0	918	1 US-08-825-558-6
16	212.5	11.0	918	2 US-09-312-611-6
17	212.5	11.0	918	2 US-09-943-180B-3
18	212.5	11.0	918	2 US-09-949-002-333
19	211.5	10.9	708	1 US-07-797-556-2
20	211.5	10.9	708	1 US-07-808-814
21	211.5	10.9	708	1 US-09-058-263-2
22	211.5	10.9	708	1 US-09-939-029-992
23	211.5	10.9	708	2 US-09-058-264-2
24	211.5	10.9	708	2 US-09-455-62-2
25	211.5	10.9	708	4 PCT-US93-06530-2
26	211.5	10.9	937	2 US-09-949-002-536
27	207.5	10.7	488	1 US-08-599-455B-5
28	207.5	10.7	488	2 US-09-069-781B-5
29	207.5	10.7	488	2 US-09-137-132-5
30	207.5	10.7	488	2 US-09-864-56A-5
31	207.5	10.7	488	2 US-09-944-410-5
32	207.5	10.7	488	2 US-08-708-123D-5
33	207.5	10.7	488	2 US-08-583-133A-5
34	207.5	10.7	488	2 US-08-638-52AB-5
35	207.5	10.7	1158	2 US-09-313-942-26
36	207.5	10.7	1158	2 US-10-282-162-26
37	207.5	10.7	1168	2 US-09-313-942-24
38	207.5	10.7	1168	2 US-10-282-162-24
39	186.5	9.6	837	1 US-07-923-976-2
40	182	9.4	1001	1 US-07-977-555-6
41	182	9.4	1001	1 US-07-943-843-2
42	182	9.4	1001	1 US-08-347-003-2
43	182	9.4	1097	1 US-07-943-843-6
44	182	9.4	1097	1 US-08-347-003-6
45	182	9.4	1097	2 US-09-949-016-6209
46	182	9.4	1119	2 US-09-949-010-10081
47	170	8.8	771	1 US-07-223-976-6
48	170	8.8	783	1 US-07-933-976-4
49	170	8.8	836	1 US-07-223-976-8
50	170	8.8	863	1 US-08-419-552-7
51	168	8.7	620	1 US-08-419-552-7
52	168	8.7	719	1 US-07-943-843-4
53	168	8.7	719	1 US-08-447-003-4
54	167	8.6	303	2 US-09-071-224-19
55	167	8.6	405	2 US-09-032-077-2
56	167	8.6	405	2 US-09-020-601-2
57	167	8.6	425	2 US-09-071-224-6
58	166.5	8.5	572	1 US-08-419-655-5
59	163.5	8.5	303	2 US-09-071-224-21
60	163.5	8.5	389	2 US-09-071-224-24
61	163.5	8.5	389	2 US-09-071-224-27
62	163.5	8.5	389	2 US-09-071-224-29
63	163.5	8.4	422	2 US-09-071-224-2
64	163	8.4	407	2 US-09-521-335-13
65	162.5	8.4	303	2 US-09-071-224-23
66	162.5	8.4	385	2 US-09-071-224-20
67	162.5	8.4	388	2 US-09-071-224-17
68	162.5	8.4	389	2 US-09-071-224-22
69	162.5	8.4	389	2 US-09-071-224-25
70	162.5	8.4	392	2 US-09-071-224-18
71	162.5	8.4	410	2 US-09-521-335-12
72	162.5	8.4	422	2 US-09-866-028-32
73	162.5	8.4	422	2 US-09-944-457-32
74	162.5	8.4	422	2 US-09-945-534-32
75	162.5	8.4	422	2 US-09-944-944-32
76	162.5	8.4	422	2 US-09-945-587-32
77	162.5	8.4	425	2 US-09-071-224-4
78	162.5	8.4	434	2 US-09-012-072-4
79	162.5	8.4	434	2 US-09-120-601-4
80	162.5	8.4	448	2 US-09-120-601-6
81	161.5	8.4	389	2 US-09-071-224-28
82	161.5	8.4	389	2 US-09-071-224-30
83	160.5	8.3	389	2 US-09-071-224-31
84	159.5	8.2	389	2 US-09-071-224-35
85	150.5	7.8	602	1 US-08-419-655-6
86	147	7.6	349	2 US-08-806-597A-14
87	147	7.6	349	2 US-08-972-428A-14
88	147	7.6	599	2 US-09-000-145-2
89	147	7.6	637	2 US-09-949-016-10128
90	138.5	7.2	623	1 US-08-53-70-07
91	138.5	7.2	623	1 US-09-073-594-7
92	138.5	7.2	623	1 US-09-215-922-7
93	136	7.0	894	1 US-08-599-455B-2
94	136	7.0	894	2 US-09-059-781B-2
95	136	7.0	894	2 US-08-518-952A-12
96	136	7.0	894	2 US-09-137-122-2
97	136	7.0	894	2 US-08-64-56A-2
98	136	7.0	894	2 US-09-054-410-2
99	136	7.0	894	2 US-08-708-123D-2
100	136	7.0	894	2 US-08-583-153A-2

ALIGNMENTS
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSE: Hoffmann-La Roche Inc.
 STREET: 340 Kingsland Street
 CITY: Nutley
 STATE: NJ
 COUNTRY: USA
 ZIP: 07110

RESULT 1
 US-09-853-180B-2
 Sequence 2, Application US/09853180B
 ; Sequence 2, Application US/08685118

GENERAL INFORMATION:

APPLICANT: Chirica, Madaline

APPLICANT: Parham, Christi L.

APPLICANT: Kastelein, Robert A.

APPLICANT: Moore, Kevin W.

TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and Methods.

FILE REFERENCE: DX01074

CURRENT APPLICATION NUMBER: US/09/853,180B

CURRENT FILING DATE: 2000-05-10

PRIOR APPLICATION NUMBER: 60/203,426

PRIOR FILING DATE: 2000-05-10

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PatentIn version 3.2

SEQ ID NO 2

LENGTH: 629

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE: misc_feature

NAME/KEY: misc_feature

LOCATION: (-21)..(-21)

OTHER INFORMATION: The 'xaa' at location -21 stands for Gln, or His.

FEATURE:

LOCATION: (126)..(126)

OTHER INFORMATION: The 'xaa' at location 126 stands for GLY, or Arg.

US-09-853-180B-2

Query Match 95.6%; Score 1868; DB 2; Length 629;
 Best Local Similarity 99.1%; Pred. No. 2.3e-176;
 Matches 345; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MNQVITQWDAVIALYKLFWSWHRGGITNINSGHIWNEPATIFKPGMGNANISYQQAIIKNCQ 60
 Db 1 MNKVTIQWDAVIALYKLFWSWHRGGITNINSGHIWNEPATIFKPGMGNANISYQQAIIKNCQ 60

Qy 32 GHIMWBPATIFKPGMGNANISYQQAIIKNCQPRKLHRYKNGIKERFOITRINKTARLYK- 90
 Db 31 GDVTVKPSHVLGTSVNTIC---SLKPR-----OGCFHYSSRNKL--ILYKF 73

Qy 91 ---NPFELPHIA-----SMYCTABCSPKHFQETLIGKDISGSGYPPDIDBVBTC 133
 Db 74 DRRINFHGHSLNSQVTLGGLGTTFLVCKLAC--INSDBIOIGARIFGVGAPEQONLSC 132

Qy 134 VIEYSGNMTCTWNAGKLVIDTKVWVH--KSLTETBESQYLTSSY---INISTDSL 186
 Db 133 IOKGBOGTVACTWERGRDTHYTYTQLSGPKNLTWQOCKDIDCYDLDGGINLTPESP 192

Qy 187 OGKXKVLWVQANALGMERSKQLOIHDIDIVTSAVISAISRAETINATVKTITWDSQT 246
 Db 193 E--SNPTAKTAVNSLIGSSSLPSTPFLDIPRPPWDIRKFOKASVRCYRDEG 250

Qy 247 TIEKVSCEMRYKATTNQWAKFEFTNTFTV--QOSEFYLEPNIKVFOURCQ-BTGKRY 303
 Db 251 LV--LNRKLYRPSNSRLWM--VNVTKAKGRIDLQKPFYEFQISSKLYKGS 304

Qy 304 WOPNWSLFFHKTPTPRTV 320
 Db 305 WSDWSESLRAQTPESP 321

RESULT 2
 US-08-685-118-2
 Sequence 2, Application US/08685118
 ; Sequence 2, Application US/08685118
 ; Patent No. 5840530
 ; GENERAL INFORMATION:
 ; APPLICANT: Gubler, Ulrich A
 ; APPLICANT: Presky, David H
 ; TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12
 ; TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12

RESULT 3
 US-08-915-495-2
 Sequence 2, Application US/08915495
 ; Sequence 2, Application US/08915495
 ; Patent No. 5852176
 ; GENERAL INFORMATION:
 ; APPLICANT: Gubler, Ulrich A
 ; APPLICANT: Presky, David H
 ; TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSE: Hoffmann-La Roche Inc.
 ; STREET: 340 Kingsland Street